



Baylor Bioinformatics

Education, Research and Future Directions

Erich Baker, Ph.D.

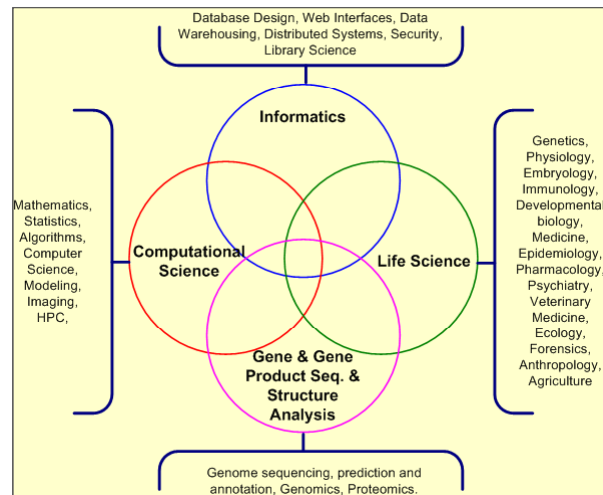


Bioinformatics at Baylor

- ▶ Bachelor of Science in Informatics, majoring in Bioinformatics
- ▶ First undergraduate program of its kind nationally (1999). Continues to occupy a very unique niche.
- ▶ There is an increasing need to train individuals at the intersection of computer science, mathematics, statistics, genetics, and chemistry.
- ▶ Approximately 40 majors.

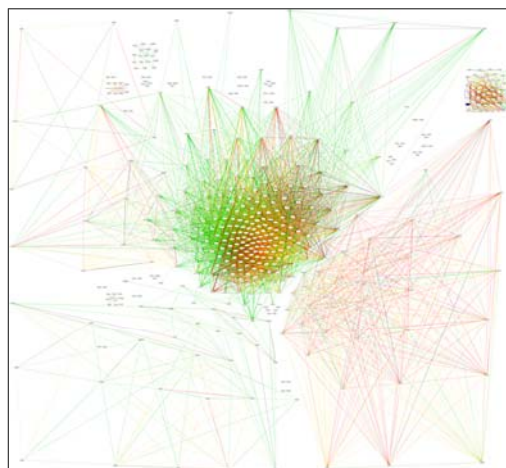


What is Bioinformatics?

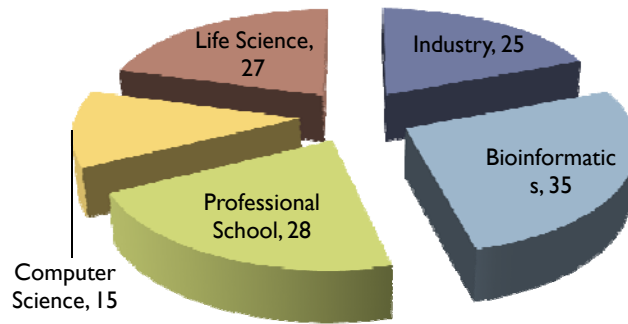


Why is Bioinformatics at Baylor Unique?

- ▶ **Computer Science**
 - ▶ 32 Hours
- ▶ **Biology**
 - ▶ 23 Hours
- ▶ **Chemistry**
 - ▶ 16 Hours
- ▶ **Bioinformatics**
 - ▶ 12 Hours
- ▶ **General Electives**
 - ▶ 0 Hours

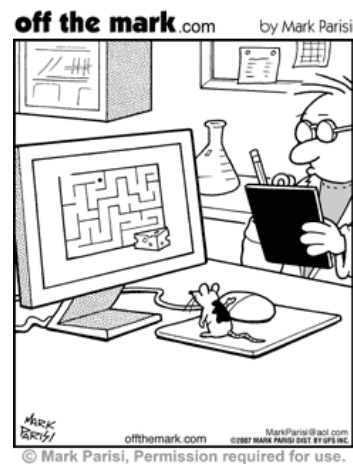


Where do our graduates go?



Research

- ▶ **Bioinformatics**
 - ▶ PTSD: managing data created by the center of excellence for traumatic brain injury. (DoD/VA)
 - ▶ INIA – MATRR. Monkey brain analysis and repository. (NIH)
 - ▶ Autism Brain Project
- ▶ **Primary Research**
 - ▶ Ontological Discovery Environment: identifying empirically created ontologies from primary biological sources. (NIH)



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Ontological Discovery Environment (ODE)

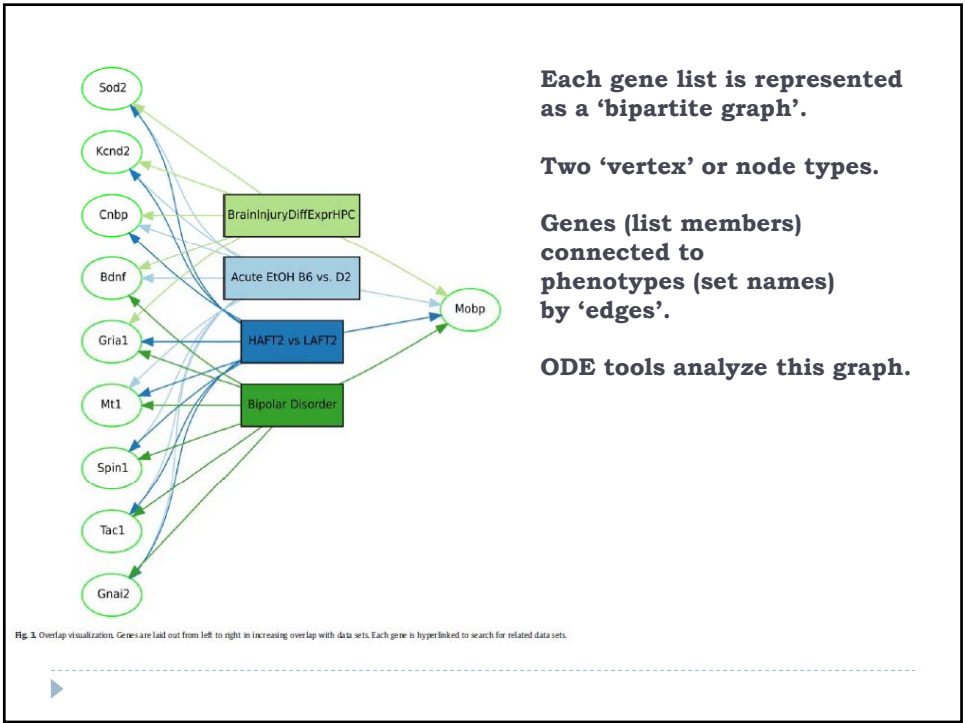
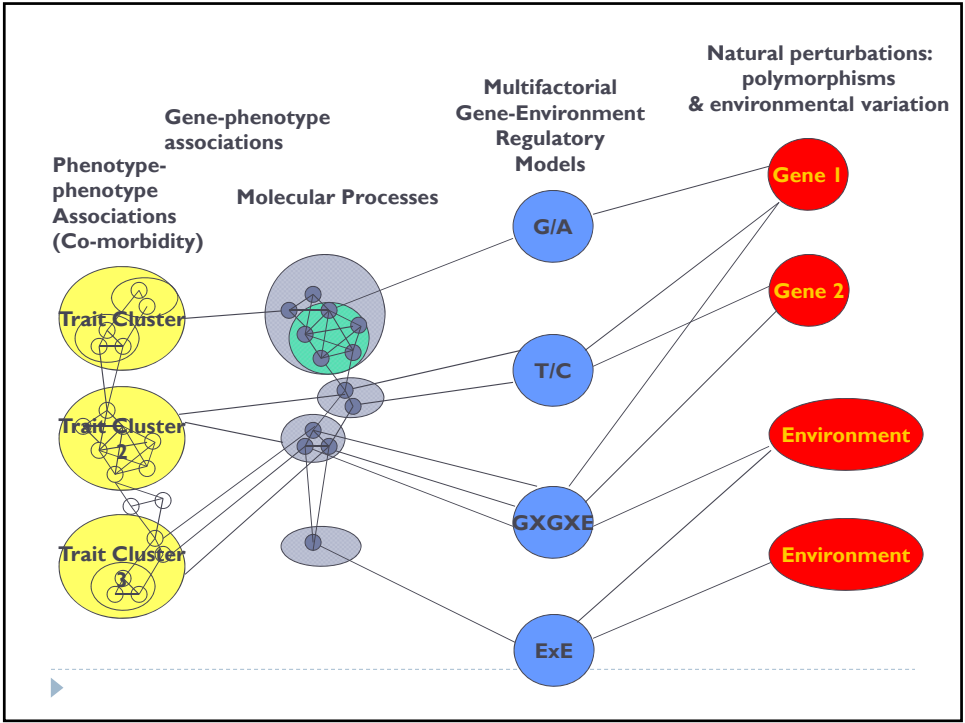
[Ontological Discovery Environment: a system for integrating gene-phenotype associations](#). Baker EJ, Jay JJ, Philip VM, Zhang Y, Li Z, Kirova R, Langston MA, Chesler EJ. *Genomics*. 2009 Dec;94(6):377-87. Epub 2009 Sep 3

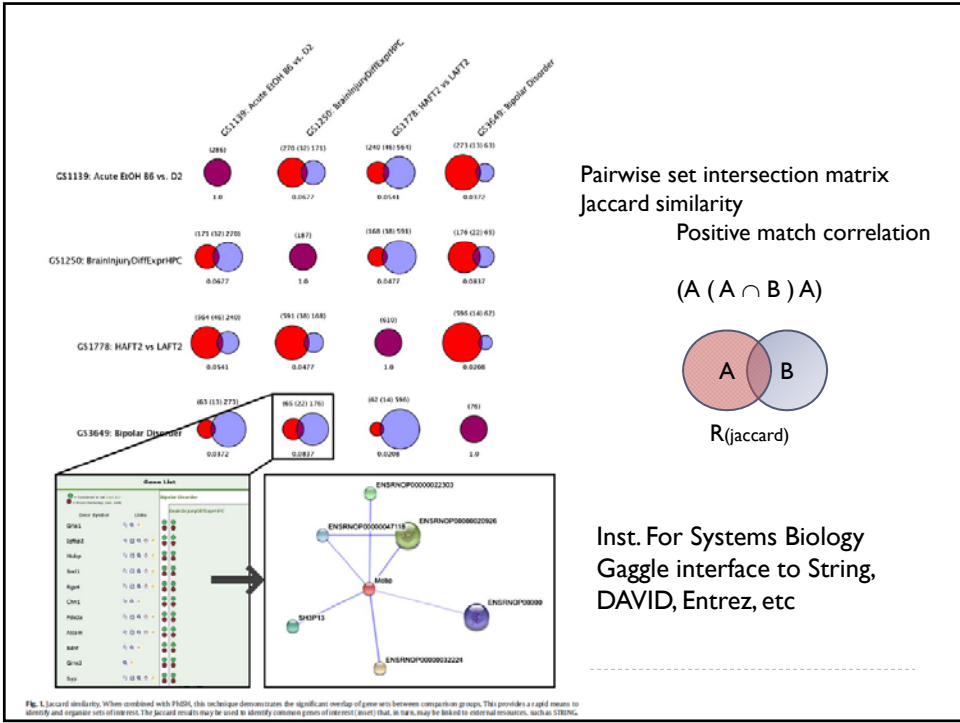


Integrative Functional Genomics

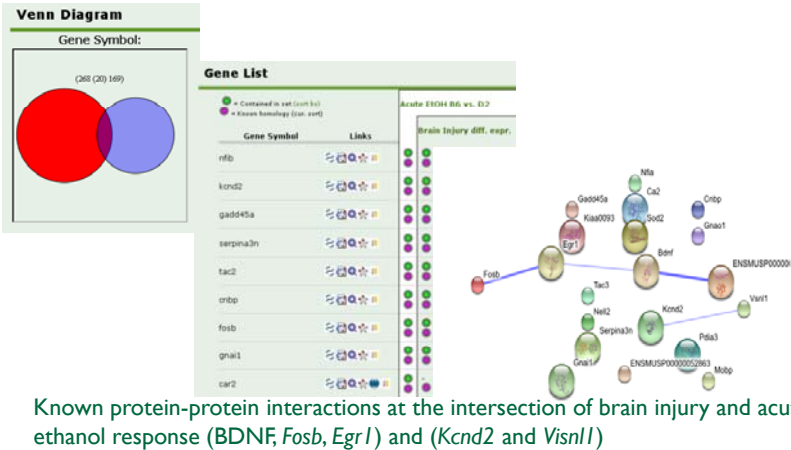
- ▶ A growing recognition of the value of integrating multiple functional genomics data sets
- ▶ Numerous available technologies for defining genes associated with highly specific functional phenomena
- ▶ Large scale integration can enable pattern recognition across multiple data sets.



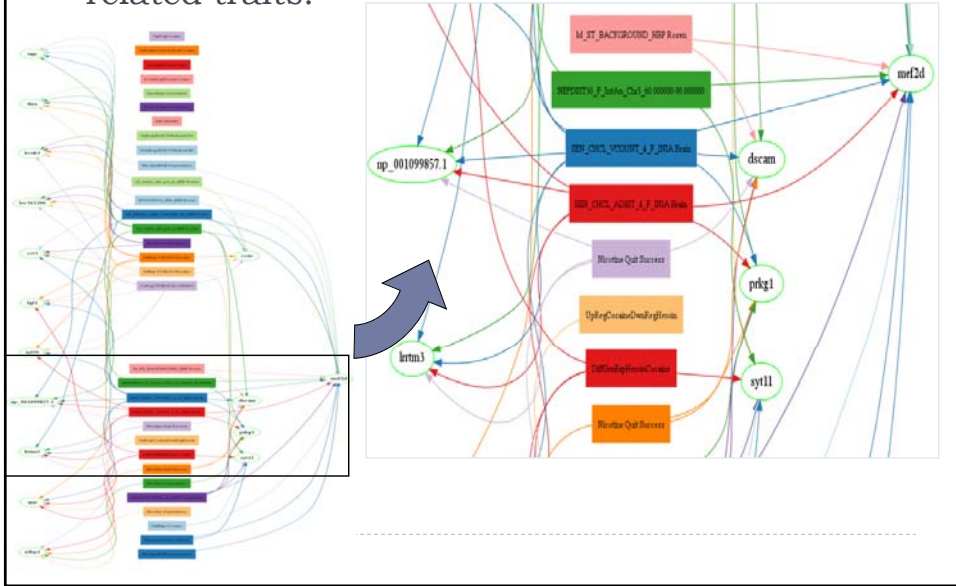




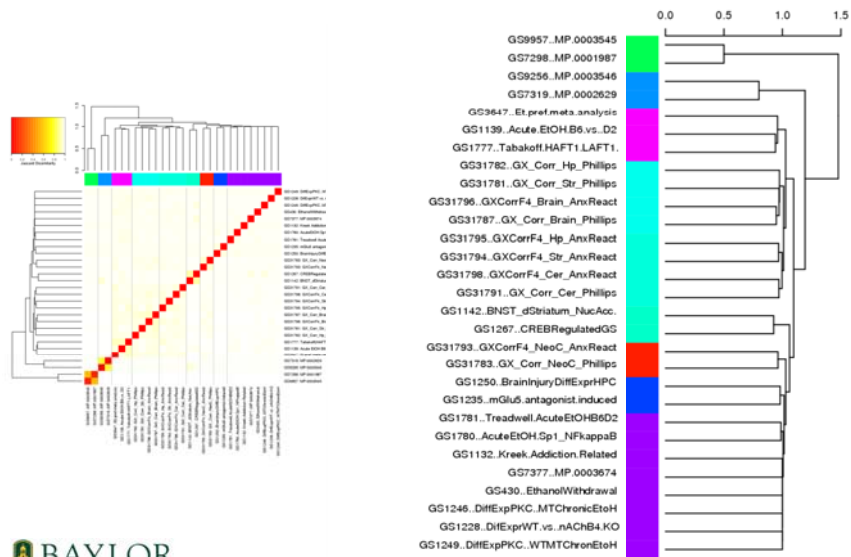
Acute alcohol response and brain injury



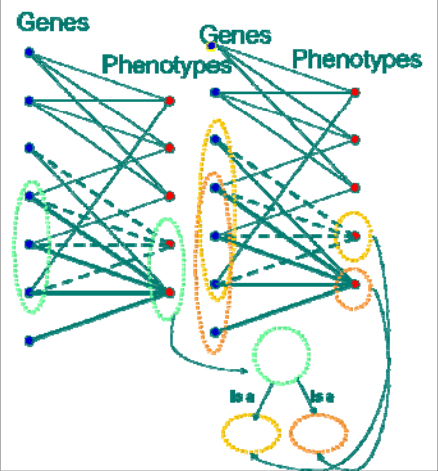
Mef2d, a cocaine sensitization candidate gene is associated with many alcohol and addiction related traits.



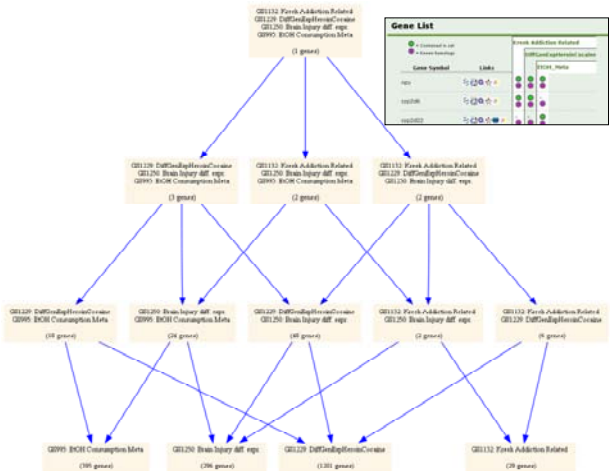
Clustering related gene sets by similarity of members



Empirical Construction of Phenotype Ontology



Inferring functional networks:
Phenotype Integration and Similarity Hierarchy (PhISH)



Defining disease categories based on biological functions

- ▶ By identifying the underlying genomic substrate of multiple phenotypes we can define categories of related and distinct traits.
- ▶ The goal is to redefine phenotypes based on the functional networks that subserve them, rather than based on overt manifestations.
- ▶ The tools of mouse genetics and genomics enable a meaningful shift from face validity to construct validity in the identification of cross-species translation of disease models.
- ▶ Finding the genes underlying these derived constructs will enable us to more directly target the biological phenomena of addiction.



Future Directions

- ▶ **Education**
 - ▶ Recruiting
 - ▶ Graduate Degrees
- ▶ **Research**
 - ▶ Department of Computer Science
 - ▶ Department of Chemistry
 - ▶ Department of Statistics
 - ▶ Department of Geology
 - ▶ Mathematics Department
 - ▶ School of Business (Medical Informatics)
 - ▶ Biology Department

